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## SEQUENCE LISTING

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&lt;211&gt; 3963

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (138)..(3068)

&lt;400&gt; 1

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Tyr	Thr	Glu	Lys	Gln	Arg	Val	Asp	Phe	Leu	Gly	Glu	Ala	Gly	Ile	Met		
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 Arg Arg Lys Asn Gln Arg Ala Arg Gln Ser Pro Glu Asp Val Tyr Phe  
 565 570 575  
 Ser Lys Ser Glu Gln Leu Lys Pro Leu Lys Thr Tyr Val Asp Pro His  
 580 585 590  
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 Gly Phe Arg Leu Pro Thr Pro Met Asp Cys Pro Ser Ala Ile Tyr Gln  
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Gly Tyr Thr Ala Ile Glu Lys Val Val Gln Met Thr Asn Asp Asp Ile		
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Lys Arg Ile Gly Val Arg Leu Pro Gly His Gln Lys Arg Ile Ala Tyr		
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<210> 9

<211> 9

<212> PRT

<213> Homo sapiens

<400> 9

Leu Leu Trp Gly Cys Ala Leu Ala Ala  
1 5

<210> 10

<211> 9

<212> PRT

<213> Homo sapiens

<400> 10

Gly Leu Thr Arg Thr Ser Val Thr Val  
1 5

<210> 11

<211> 9

<212> PRT

<213> Homo sapiens

<400> 11

Asn Leu Tyr Tyr Ala Glu Ser Asp Leu  
1 5

<210> 12  
<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 12

Lys Leu Asn Val Glu Glu Arg Ser Val  
1 5

<210> 13  
<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 13

Ile Met Gly Gln Phe Ser His His Asn  
1 5

<210> 14  
<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 14

Tyr Ser Val Cys Asn Val Met Ser Gly  
1 5

<210> 15  
<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 15

Met Gln Asn Ile Met Asn Asp Met Pro  
1 5

<210> 16  
<211> 15  
<212> PRT  
<213> Homo sapiens

<400> 16

Glu Ala Gly Ile Met Gly Gln Phe Ser His His Asn Ile Ile Arg  
1 5 10 15

<210> 17  
<211> 13  
<212> PRT  
<213> Homo sapiens

<400> 17

Pro Ile Tyr Met Tyr Ser Val Cys Asn Val Met Ser Gly  
 1 5 10

<210> 18  
 <211> 16  
 <212> PRT  
 <213> Homo sapiens

<400> 18

Asp Leu Met Gln Asn Ile Met Asn Asp Met Pro Ile Tyr Met Tyr Ser  
 1 5 10 15

<210> 19  
 <211> 3105  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion construct

<400> 19  
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 gagctccagg cagcccgcgc ctgcttcgcc ctgctgtggg gctgtgcgct ggccgcggcc 240  
 gcggcgggcg agggcaagga agtgggtactg ctggactttg ctgcagctgg aggggagctc 300  
 ggctgggtca cacaccgta tggcaaaggg tgggacctga tgcagaacat catgaatgac 360  
 atgccgatct acatgtactc cgtgtgcaac gtgatgtctg gcgaccagga caactggctc 420  
 cgcaccaact ggggtgtaccg aggagaggct gagcgtatct tcattgagct caagtttact 480  
 gtacgtgact gcaacagctt ccctgggtggc gccagctcct gcaaggagac tttcaacctc 540  
 tactatgccg agtcggacct ggactacggc accaacttcc agaagcgcct gttcaccaag 600  
 attgacacca ttgcgcccga tgagatcacc gtcagcagcg acttcgaggc acgccacgtg 660  
 aagctgaacg tggaggagcg ctccgtgggg ccgctcaccg gcaaaggctt ctacctggcc 720  
 ttccaggata tcggtgcctg tgtggcgctg ctctccgtcc gtgtctacta caagaagtgc 780  
 cccgagctgc tgcagggcct ggcccacttc cctgagacca tcgccggctc tgatgcacct 840  
 tccctggcca ctgtggccgg cacctgtgtg gaccatgccg tggtgccacc ggggggtgaa 900  
 gagccccgta tgcactgtgc agtggatggc gagtggctgg tgcccattgg gcagtgcctg 960  
 tgccaggcag gctacgagaa ggtggaggat gcctgccagg cctgctcgcc tggatttttt 1020  
 aagtttgagg catctgagag ccctgcttg gagtgccttg agcacacgct gccatccctt 1080

gaggggtgcca	cctcctgcga	gtgtgaggaa	ggcttcttcc	gggcacctca	ggacccagcg	1140
tcgatgcctt	gcacacgacc	cccctccgcc	ccacactacc	tcacagccgt	gggcatgggt	1200
gccaaggtgg	agctgcgctg	gacgccccct	caggacagcg	ggggccgcga	ggacattgtc	1260
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cagcagagcc	gagtgtggaa	gtacgaggtc	acttaccgca	agaagggaga	ctccaacagc	1620
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ttgaagttca	ctaccgagat	ccatccatcc	tgtgtcactc	ggcagaaggt	gatcggagca	2040
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ccggtggcca	tcaagacgct	gaaagccggc	tacacagaga	agcagcgagt	ggacttcctc	2160
ggcgaggccg	gcatcatggg	ccagttcagc	caccacaaca	tcacccgcct	agagggcgtc	2220
atctccaaat	acaagcccat	gatgatcatc	actgagtaca	tggagaatgg	ggccctggac	2280
aagttccttc	gggagaagga	tggcgagttc	agcgtgctgc	agctggtggg	catgctgcgg	2340
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gcccgaaca	tcctcgtcaa	cagcaacctg	gtctgcaagg	tgtctgactt	tggcctgtcc	2460
cgcgtgctgg	aggacgaccc	cgaggccacc	tacaccacca	gtggcggcaa	gatccccatc	2520
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tccaaccacg	aggtgatgaa	agccatcaat	gatggcttcc	ggctccccac	acccatggac	2700
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cccaagttcg	ctgacatcgt	cagcatcctg	gacaagctca	ttcgtgcccc	tgactccctc	2820
aagaccctgg	ctgactttga	ccccgcgtg	tctatccggc	tccccagcac	gagcggctcg	2880
gaggggggtgc	ccttccgcac	ggtgtccgag	tggctggagt	ccatcaagat	gcagcagtat	2940

acggagcact tcattggcggc cggctacact gccatcgaga aggtggtgca gatgaccaac 3000  
gacgacatca agaggattgg ggtgcggctg cccggccacc agaagcgcat cgcctacagc 3060  
ctgctgggac tcaaggacca ggtgaacact gtggggatcc ccatac 3105

<210> 20  
<211> 1035  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Predicted fusion protein

<400> 20

Met	Lys	Lys	Ile	Met	Leu	Val	Phe	Ile	Thr	Leu	Ile	Leu	Val	Ser	Leu	1	5	10	15
Pro	Ile	Ala	Gln	Gln	Thr	Glu	Ala	Lys	Asp	Ala	Ser	Ala	Phe	Asn	Lys	20	25	30	
Glu	Asn	Ser	Ile	Ser	Ser	Met	Ala	Pro	Pro	Ala	Ser	Pro	Pro	Ala	Ser	35	40	45	
Pro	Lys	Thr	Pro	Ile	Glu	Lys	Lys	His	Ala	Asp	Leu	Glu	Leu	Gln	Ala	50	55	60	
Ala	Arg	Ala	Cys	Phe	Ala	Leu	Leu	Trp	Gly	Cys	Ala	Leu	Ala	Ala	Ala	65	70	75	80
Ala	Ala	Ala	Gln	Gly	Lys	Glu	Val	Val	Leu	Leu	Asp	Phe	Ala	Ala	Ala	85	90	95	
Gly	Gly	Glu	Leu	Gly	Trp	Leu	Thr	His	Pro	Tyr	Gly	Lys	Gly	Trp	Asp	100	105	110	
Leu	Met	Gln	Asn	Ile	Met	Asn	Asp	Met	Pro	Ile	Tyr	Met	Tyr	Ser	Val	115	120	125	
Cys	Asn	Val	Met	Ser	Gly	Asp	Gln	Asp	Asn	Trp	Leu	Arg	Thr	Asn	Trp	130	135	140	
Val	Tyr	Arg	Gly	Glu	Ala	Glu	Arg	Ile	Phe	Ile	Glu	Leu	Lys	Phe	Thr	145	150	155	160
Val	Arg	Asp	Cys	Asn	Ser	Phe	Pro	Gly	Gly	Ala	Ser	Ser	Cys	Lys	Glu	165	170	175	
Thr	Phe	Asn	Leu	Tyr	Tyr	Ala	Glu	Ser	Asp	Leu	Asp	Tyr	Gly	Thr	Asn	180	185	190	
Phe	Gln	Lys	Arg	Leu	Phe	Thr	Lys	Ile	Asp	Thr	Ile	Ala	Pro	Asp	Glu	195	200	205	
Ile	Thr	Val	Ser	Ser	Asp	Phe	Glu	Ala	Arg	His	Val	Lys	Leu	Asn	Val	210	215	220	
Glu	Glu	Arg	Ser	Val	Gly	Pro	Leu	Thr	Arg	Lys	Gly	Phe	Tyr	Leu	Ala				

225						230						235						240
Phe	Gln	Asp	Ile	Gly	Ala	Cys	Val	Ala	Leu	Leu	Ser	Val	Arg	Val	Tyr			
				245					250					255				
Tyr	Lys	Lys	Cys	Pro	Glu	Leu	Leu	Gln	Gly	Leu	Ala	His	Phe	Pro	Glu			
			260					265					270					
Thr	Ile	Ala	Gly	Ser	Asp	Ala	Pro	Ser	Leu	Ala	Thr	Val	Ala	Gly	Thr			
		275					280					285						
Cys	Val	Asp	His	Ala	Val	Val	Pro	Pro	Gly	Gly	Glu	Glu	Pro	Arg	Met			
	290					295					300							
His	Cys	Ala	Val	Asp	Gly	Glu	Trp	Leu	Val	Pro	Ile	Gly	Gln	Cys	Leu			
305					310					315					320			
Cys	Gln	Ala	Gly	Tyr	Glu	Lys	Val	Glu	Asp	Ala	Cys	Gln	Ala	Cys	Ser			
				325					330					335				
Pro	Gly	Phe	Phe	Lys	Phe	Glu	Ala	Ser	Glu	Ser	Pro	Cys	Leu	Glu	Cys			
			340					345					350					
Pro	Glu	His	Thr	Leu	Pro	Ser	Pro	Glu	Gly	Ala	Thr	Ser	Cys	Glu	Cys			
		355					360					365						
Glu	Glu	Gly	Phe	Phe	Arg	Ala	Pro	Gln	Asp	Pro	Ala	Ser	Met	Pro	Cys			
	370					375					380							
Thr	Arg	Pro	Pro	Ser	Ala	Pro	His	Tyr	Leu	Thr	Ala	Val	Gly	Met	Gly			
385					390					395					400			
Ala	Lys	Val	Glu	Leu	Arg	Trp	Thr	Pro	Pro	Gln	Asp	Ser	Gly	Gly	Arg			
				405					410					415				
Glu	Asp	Ile	Val	Tyr	Ser	Val	Thr	Cys	Glu	Gln	Cys	Trp	Pro	Glu	Ser			
		420						425					430					
Gly	Glu	Cys	Gly	Pro	Cys	Glu	Ala	Ser	Val	Arg	Tyr	Ser	Glu	Pro	Pro			
		435					440					445						
His	Gly	Leu	Thr	Arg	Thr	Ser	Val	Thr	Val	Ser	Asp	Leu	Glu	Pro	His			
	450					455					460							
Met	Asn	Tyr	Thr	Phe	Thr	Val	Glu	Ala	Arg	Asn	Gly	Val	Ser	Gly	Leu			
465					470					475					480			
Val	Thr	Ser	Arg	Ser	Phe	Arg	Thr	Ala	Ser	Val	Ser	Ile	Asn	Gln	Thr			
				485					490					495				
Glu	Pro	Pro	Lys	Val	Arg	Leu	Glu	Gly	Arg	Ser	Thr	Thr	Ser	Leu	Ser			
			500					505					510					
Val	Ser	Trp	Ser	Ile	Pro	Pro	Pro	Gln	Gln	Ser	Arg	Val	Trp	Lys	Tyr			
		515					520					525						
Glu	Val	Thr	Tyr	Arg	Lys	Lys	Gly	Asp	Ser	Asn	Ser	Tyr	Asn	Val	Arg			
	530					535					540							
Arg	Thr	Glu	Gly	Phe	Ser	Val	Thr	Leu	Asp	Asp	Leu	Ala	Pro	Asp	Thr			
545					550					555					560			

Thr	Tyr	Leu	Val	Gln	Val	Gln	Ala	Leu	Thr	Gln	Glu	Gly	Gln	Gly	Ala	
				565					570						575	
Gly	Ser	Arg	Val	His	Glu	Phe	Gln	Thr	Leu	Ser	Pro	Glu	Gly	Ser	Gly	
			580					585					590			
Asn	Leu	Ala	Val	Ile	Gly	Gly	Val	Ala	Val	Gly	Val	Val	Leu	Leu	Leu	
		595					600					605				
Val	Leu	Ala	Gly	Val	Gly	Phe	Phe	Ile	His	Arg	Arg	Arg	Lys	Asn	Gln	
	610					615					620					
Arg	Ala	Arg	Gln	Ser	Pro	Glu	Asp	Val	Tyr	Phe	Ser	Lys	Ser	Glu	Gln	
	625				630					635					640	
Leu	Lys	Pro	Leu	Lys	Thr	Tyr	Val	Asp	Pro	His	Thr	Tyr	Glu	Asp	Pro	
				645					650					655		
Asn	Gln	Ala	Val	Leu	Lys	Phe	Thr	Thr	Glu	Ile	His	Pro	Ser	Cys	Val	
			660					665						670		
Thr	Arg	Gln	Lys	Val	Ile	Gly	Ala	Gly	Glu	Phe	Gly	Glu	Val	Tyr	Lys	
		675					680					685				
Gly	Met	Leu	Lys	Thr	Ser	Ser	Gly	Lys	Lys	Glu	Val	Pro	Val	Ala	Ile	
	690					695					700					
Lys	Thr	Leu	Lys	Ala	Gly	Tyr	Thr	Glu	Lys	Gln	Arg	Val	Asp	Phe	Leu	
	705				710					715					720	
Gly	Glu	Ala	Gly	Ile	Met	Gly	Gln	Phe	Ser	His	His	Asn	Ile	Ile	Arg	
				725					730					735		
Leu	Glu	Gly	Val	Ile	Ser	Lys	Tyr	Lys	Pro	Met	Met	Ile	Ile	Thr	Glu	
			740					745					750			
Tyr	Met	Glu	Asn	Gly	Ala	Leu	Asp	Lys	Phe	Leu	Arg	Glu	Lys	Asp	Gly	
		755					760					765				
Glu	Phe	Ser	Val	Leu	Gln	Leu	Val	Gly	Met	Leu	Arg	Gly	Ile	Ala	Ala	
	770					775					780					
Gly	Met	Lys	Tyr	Leu	Ala	Asn	Met	Asn	Tyr	Val	His	Arg	Asp	Leu	Ala	
	785				790					795					800	
Ala	Arg	Asn	Ile	Leu	Val	Asn	Ser	Asn	Leu	Val	Cys	Lys	Val	Ser	Asp	
				805					810					815		
Phe	Gly	Leu	Ser	Arg	Val	Leu	Glu	Asp	Asp	Pro	Glu	Ala	Thr	Tyr	Thr	
			820					825					830			
Thr	Ser	Gly	Gly	Lys	Ile	Pro	Ile	Arg	Trp	Thr	Ala	Pro	Glu	Ala	Ile	
		835					840					845				
Ser	Tyr	Arg	Lys	Phe	Thr	Ser	Ala	Ser	Asp	Val	Trp	Ser	Phe	Gly	Ile	
	850					855					860					
Val	Met	Trp	Glu	Val	Met	Thr	Tyr	Gly	Glu	Arg	Pro	Tyr	Trp	Glu	Leu	
	865				870					875					880	



Ser Asn His Glu Val Met Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro  
 885 890 895  
 Thr Pro Met Asp Cys Pro Ser Ala Ile Tyr Gln Leu Met Met Gln Cys  
 900 905 910  
 Trp Gln Gln Glu Arg Ala Arg Arg Pro Lys Phe Ala Asp Ile Val Ser  
 915 920 925  
 Ile Leu Asp Lys Leu Ile Arg Ala Pro Asp Ser Leu Lys Thr Leu Ala  
 930 935 940  
 Asp Phe Asp Pro Arg Val Ser Ile Arg Leu Pro Ser Thr Ser Gly Ser  
 945 950 955 960  
 Glu Gly Val Pro Phe Arg Thr Val Ser Glu Trp Leu Glu Ser Ile Lys  
 965 970 975  
 Met Gln Gln Tyr Thr Glu His Phe Met Ala Ala Gly Tyr Thr Ala Ile  
 980 985 990  
 Glu Lys Val Val Gln Met Thr Asn Asp Asp Ile Lys Arg Ile Gly Val  
 995 1000 1005  
 Arg Leu Pro Gly His Gln Lys Arg Ile Ala Tyr Ser Leu Leu Gly  
 1010 1015 1020  
 Leu Lys Asp Gln Val Asn Thr Val Gly Ile Pro Ile  
 1025 1030 1035

<210> 21  
 <211> 1506  
 <212> DNA  
 <213> Homo sapiens

<400> 21  
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 acacacccgt atggcaaagg gtgggacctg atgcagaaca tcatgaatga catgccgatc 120  
 tacatgtact ccgtgtgcaa cgtgatgtct ggcgaccagg acaactggct ccgcaccaac 180  
 tgggtgtacc gaggagaggc tgagcgtatc ttcattgagc tcaagtttac tgtacgtgac 240  
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 gagtgggacc tggactacgg caccaacttc cagaagcgcc tgttcaccaa gattgacacc 360  
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ggctacgaga aggtggagga tgcctgccag gcctgctcgc ctggattttt taagtttgag	780
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gagctgcgct ggacgcccc tcaggacagc gggggccgcg aggacattgt ctacagcgtc	1020
acctgcgaac agtgctggcc cgagtctggg gaatgcgggc cgtgtgaggc cagtgtgcgc	1080
tactcggagc ctctcacgg actgaccgc accagtgtga cagtgagcga cctggagccc	1140
cacatgaact acaccttcac cgtggaggcc cgcaatggcg tctcaggcct ggtaaccagc	1200
cgcagcttcc gtactgccag tgtcagcatc aaccagacag agcccccaa ggtgaggctg	1260
gagggccgca gcaccacctc gcttagcgtc tcttgagca tcccccgcc gcagcagagc	1320
cgagtgtgga agtacgaggt cacttaccgc aagaaggag actccaacag ctacaatgtg	1380
cgcgcaccg agggtttctc cgtgaccctg gacgacctg cccagacac cacctacctg	1440
gtccagggtgc aggcactgac gcaggagggc cagggggccg gcagcagggt gcacgaattc	1500
cagacg	1506

<210> 22  
 <211> 1506  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Human sequence optimized for codon usage in Listeria

<400> 22	
caaggtaaag aagttgtttt attagatttt gcagcagcag gtggtgaatt aggttggtta	60
acacatccat atggtaaagg ttgggattta atgcaaaata ttatgaatga tatgccaatt	120
tatatgtata gtgtttgtaa tgttatgagt ggtgatcaag ataattggtt acgtacaaat	180
tgggtttatc gtggtgaagc agaacgtatt tttattgaat taaaatttac agttcgtgat	240
tgtaatagtt ttccagggtg tgcaagtagt tgtaaagaaa catttaattt atattatgca	300
gaaagtgatt tagattatgg tacaaatttt caaaaacggt tattttacaaa aattgataca	360
attgcaccag atgaaattac agttagtagt gattttgaag cacgtcatgt taaattaaat	420
gttgaagaac gtagtggttg tccattaaca cgtaaagggt tttatttagc atttcaagat	480
attggtgcat gtgttgcatt attaagtgtt cgtgtttatt ataaaaaatg tccagaatta	540
ttacaagggt tagcacattt tccagaaaca attgcaggta gtgatgcacc aagtttagca	600
acagttgcag gtacatgtgt tgatcatgca gttgttccac caggtggtga agaaccacgt	660

atgcattgtg cagttgatgg tgaatggta gttccaattg gtcaatgttt atgtcaagca 720  
 ggttatgaaa aagttgaaga tgcattgtcaa gcatgtagtc cagggtttttt taaatttgaa 780  
 gcaagtgaaa gtccatgttt agaattgtcca gaacatacat taccaagtcc agaagggtgca 840  
 acaagttgtg aatgtgaaga aggttttttt cgtgcaccac aagatccagc aagtatgcca 900  
 tgtacacgtc caccaagtgc accacattat ttaacagcag ttggtatggg tgcaaaagtt 960  
 gaattacgtt ggacaccacc acaagatagt ggtggtcgtg aagatattgt ttatagtgtt 1020  
 acatgtgaac aatgttggcc agaaagtggg gaatgtggtc catgtgaagc aagtgttcgt 1080  
 tatagtgaac caccacatgg tttaacacgt acaagtgtta cagttagtga tttagaacca 1140  
 catatgaatt atacatttac agttgaagca cgtaatgggtg ttagtggttt agttacaagt 1200  
 cgtagttttc gtacagcaag tgtagtatt aatcaaacag aaccaccaa agttcgttta 1260  
 gaaggtcgta gtacaacaag tttaagtgtt agttggagta ttccaccacc acaacaaagt 1320  
 cgtgttttga aatatgaagt tacatatcgt aaaaaaggtg atagtaatag ttataatgtt 1380  
 cgtcgtacag aagggttttag tgttacatta gatgatttag caccagatac aacatattta 1440  
 gttcaagttc aagcattaac acaagaaggt caagggtgcag gtagtcgtgt tcatgaattt 1500  
 caaaca 1506

<210> 23  
 <211> 502  
 <212> PRT  
 <213> Homo sapeins

<400> 23

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 Leu Gly Trp Leu Thr His Pro Tyr Gly Lys Gly Trp Asp Leu Met Gln  
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 Asn Ile Met Asn Asp Met Pro Ile Tyr Met Tyr Ser Val Cys Asn Val  
 35 40 45  
 Met Ser Gly Asp Gln Asp Asn Trp Leu Arg Thr Asn Trp Val Tyr Arg  
 50 55 60  
 Gly Glu Ala Glu Arg Ile Phe Ile Glu Leu Lys Phe Thr Val Arg Asp  
 65 70 75 80  
 Cys Asn Ser Phe Pro Gly Gly Ala Ser Ser Cys Lys Glu Thr Phe Asn  
 85 90 95  
 Leu Tyr Tyr Ala Glu Ser Asp Leu Asp Tyr Gly Thr Asn Phe Gln Lys  
 100 105 110  
 Arg Leu Phe Thr Lys Ile Asp Thr Ile Ala Pro Asp Glu Ile Thr Val  
 115 120 125

Ser	Ser	Asp	Phe	Glu	Ala	Arg	His	Val	Lys	Leu	Asn	Val	Glu	Glu	Arg	130	135	140
Ser	Val	Gly	Pro	Leu	Thr	Arg	Lys	Gly	Phe	Tyr	Leu	Ala	Phe	Gln	Asp	145	150	155
Ile	Gly	Ala	Cys	Val	Ala	Leu	Leu	Ser	Val	Arg	Val	Tyr	Tyr	Lys	Lys	165	170	175
Cys	Pro	Glu	Leu	Leu	Gln	Gly	Leu	Ala	His	Phe	Pro	Glu	Thr	Ile	Ala	180	185	190
Gly	Ser	Asp	Ala	Pro	Ser	Leu	Ala	Thr	Val	Ala	Gly	Thr	Cys	Val	Asp	195	200	205
His	Ala	Val	Val	Pro	Pro	Gly	Gly	Glu	Glu	Pro	Arg	Met	His	Cys	Ala	210	215	220
Val	Asp	Gly	Glu	Trp	Leu	Val	Pro	Ile	Gly	Gln	Cys	Leu	Cys	Gln	Ala	225	230	235
Gly	Tyr	Glu	Lys	Val	Glu	Asp	Ala	Cys	Gln	Ala	Cys	Ser	Pro	Gly	Phe	245	250	255
Phe	Lys	Phe	Glu	Ala	Ser	Glu	Ser	Pro	Cys	Leu	Glu	Cys	Pro	Glu	His	260	265	270
Thr	Leu	Pro	Ser	Pro	Glu	Gly	Ala	Thr	Ser	Cys	Glu	Cys	Glu	Glu	Gly	275	280	285
Phe	Phe	Arg	Ala	Pro	Gln	Asp	Pro	Ala	Ser	Met	Pro	Cys	Thr	Arg	Pro	290	295	300
Pro	Ser	Ala	Pro	His	Tyr	Leu	Thr	Ala	Val	Gly	Met	Gly	Ala	Lys	Val	305	310	315
Glu	Leu	Arg	Trp	Thr	Pro	Pro	Gln	Asp	Ser	Gly	Gly	Arg	Glu	Asp	Ile	325	330	335
Val	Tyr	Ser	Val	Thr	Cys	Glu	Gln	Cys	Trp	Pro	Glu	Ser	Gly	Glu	Cys	340	345	350
Gly	Pro	Cys	Glu	Ala	Ser	Val	Arg	Tyr	Ser	Glu	Pro	Pro	His	Gly	Leu	355	360	365
Thr	Arg	Thr	Ser	Val	Thr	Val	Ser	Asp	Leu	Glu	Pro	His	Met	Asn	Tyr	370	375	380
Thr	Phe	Thr	Val	Glu	Ala	Arg	Asn	Gly	Val	Ser	Gly	Leu	Val	Thr	Ser	385	390	395
Arg	Ser	Phe	Arg	Thr	Ala	Ser	Val	Ser	Ile	Asn	Gln	Thr	Glu	Pro	Pro	405	410	415
Lys	Val	Arg	Leu	Glu	Gly	Arg	Ser	Thr	Thr	Ser	Leu	Ser	Val	Ser	Trp	420	425	430
Ser	Ile	Pro	Pro	Pro	Gln	Gln	Ser	Arg	Val	Trp	Lys	Tyr	Glu	Val	Thr	435	440	445

Tyr Arg Lys Lys Gly Asp Ser Asn Ser Tyr Asn Val Arg Arg Thr Glu  
 450 455 460  
 Gly Phe Ser Val Thr Leu Asp Asp Leu Ala Pro Asp Thr Thr Tyr Leu  
 465 470 475 480  
 Val Gln Val Gln Ala Leu Thr Gln Glu Gly Gln Gly Ala Gly Ser Arg  
 485 490 495  
 Val His Glu Phe Gln Thr  
 500

<210> 24  
 <211> 1689  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion protein construct

<400> 24  
 atgaaaaaaa taatgctagt ttttattaca cttatattag ttagtctacc aattgcgcaa 60  
 caaactgaag caaaggatgc atctgcattc aataaagaaa attcaatttc atccatggca 120  
 ccaccagcat ctccgcctgc aagtcctaag acgccaatcg aaaagaaaca cgcggatctc 180  
 gagcagggca aggaagtggc actgctggac tttgctgcag ctggagggga gctcggctgg 240  
 ctcacacacc cgtatggcaa aggggtgggac ctgatgcaga acatcatgaa tgacatgccg 300  
 atctacatgt actccgtgtg caacgtgatg tctggcgacc aggacaactg gctccgcacc 360  
 aactgggtgt accgaggaga ggctgagcgt atcttcattg agctcaagtt tactgtacgt 420  
 gactgcaaca gcttccctgg tggcgccagc tcctgcaagg agactttcaa cctctactat 480  
 gccgagtcgg acctggacta cggcaccaac ttccagaagc gcctgttcac caagattgac 540  
 accattgcgc ccgatgagat caccgtcagc agcgacttcg aggcacgcca cgtgaagctg 600  
 aacgtggagg agcgctccgt ggggccgctc acccgcaaag gcttctacct ggccttcag 660  
 gatatcgggtg cctgtgtggc gctgctctcc gtccgtgtct actacaagaa gtgccccgag 720  
 ctgctgcagg gcctggccca cttccctgag accatcgccg gctctgatgc accttccctg 780  
 gccactgtgg ccggcacctg tgtggacat gccgtggtgc caccgggggg tgaagagccc 840  
 cgtatgcact gtgcagtgga tggcgagtgg ctggtgcca ttgggcagtg cctgtgccag 900  
 gcaggctaag agaaggtgga ggatgcctgc caggcctgct cgctgggatt ttttaagttt 960  
 gaggcattctg agagcccctg cttggagtgc cctgagcaca cgctgccatc ccctgagggt 1020  
 gccacctcct gcgagtgtga ggaaggcttc ttccgggcac ctccaggacc agcgtcgatg 1080  
 ccttgacacac gacccccctc cgccccacac tacctcacag ccgtgggcat gggtgccaag 1140  
 gtggagctgc gctggacgcc ccctcaggac agcggggggc gcgaggacat tgtctacagc 1200

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gtcacctgcg aacagtgtg gcccgagtct ggggaatgcg ggccgtgtga ggccagtgtg 1260
cgctactcgg agcctcctca cggactgacc cgcaccagtg tgacagttag cgacctggag 1320
ccccacatga actacacctt caccgtggag gcccgcaatg gcgtctcagg cctggtaacc 1380
agccgcagct tccgtactgc cagtgtcagc atcaaccaga cagagcccc caaggtgagg 1440
ctggagggcc gcagcaccac ctcgcttagc gtctcctgga gcatcccccc gccgcagcag 1500
agccgagtgt ggaagtacga ggtcacttac cgcaagaagg gagactccaa cagctacaat 1560
gtgcgccgca ccgaggggtt ctccgtgacc ctggacgacc tggccccaga caccacctac 1620
ctggtccagg tgcaggcact gacgcaggag ggccaggggg ccggcagcag ggtgcacgaa 1680
ttccagacg 1689

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<210> 25
<211> 563
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Predicted fusion protein

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<400> 25

```

```

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
1           5           10           15
Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
          20           25           30
Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser
          35           40           45
Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Leu Glu Gln Gly Lys
          50           55           60
Glu Val Val Leu Leu Asp Phe Ala Ala Ala Gly Gly Glu Leu Gly Trp
65           70           75           80
Leu Thr His Pro Tyr Gly Lys Gly Trp Asp Leu Met Gln Asn Ile Met
          85           90           95
Asn Asp Met Pro Ile Tyr Met Tyr Ser Val Cys Asn Val Met Ser Gly
          100          105          110
Asp Gln Asp Asn Trp Leu Arg Thr Asn Trp Val Tyr Arg Gly Glu Ala
          115          120          125
Glu Arg Ile Phe Ile Glu Leu Lys Phe Thr Val Arg Asp Cys Asn Ser
          130          135          140
Phe Pro Gly Gly Ala Ser Ser Cys Lys Glu Thr Phe Asn Leu Tyr Tyr
          145          150          155          160
Ala Glu Ser Asp Leu Asp Tyr Gly Thr Asn Phe Gln Lys Arg Leu Phe

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165					170					175					
Thr	Lys	Ile	Asp	Thr	Ile	Ala	Pro	Asp	Glu	Ile	Thr	Val	Ser	Ser	Asp
			180					185					190		
Phe	Glu	Ala	Arg	His	Val	Lys	Leu	Asn	Val	Glu	Glu	Arg	Ser	Val	Gly
		195					200					205			
Pro	Leu	Thr	Arg	Lys	Gly	Phe	Tyr	Leu	Ala	Phe	Gln	Asp	Ile	Gly	Ala
	210					215					220				
Cys	Val	Ala	Leu	Leu	Ser	Val	Arg	Val	Tyr	Tyr	Lys	Lys	Cys	Pro	Glu
225					230					235					240
Leu	Leu	Gln	Gly	Leu	Ala	His	Phe	Pro	Glu	Thr	Ile	Ala	Gly	Ser	Asp
				245					250					255	
Ala	Pro	Ser	Leu	Ala	Thr	Val	Ala	Gly	Thr	Cys	Val	Asp	His	Ala	Val
			260					265					270		
Val	Pro	Pro	Gly	Gly	Glu	Glu	Pro	Arg	Met	His	Cys	Ala	Val	Asp	Gly
		275					280					285			
Glu	Trp	Leu	Val	Pro	Ile	Gly	Gln	Cys	Leu	Cys	Gln	Ala	Gly	Tyr	Glu
	290					295					300				
Lys	Val	Glu	Asp	Ala	Cys	Gln	Ala	Cys	Ser	Pro	Gly	Phe	Phe	Lys	Phe
305					310					315					320
Glu	Ala	Ser	Glu	Ser	Pro	Cys	Leu	Glu	Cys	Pro	Glu	His	Thr	Leu	Pro
				325					330					335	
Ser	Pro	Glu	Gly	Ala	Thr	Ser	Cys	Glu	Cys	Glu	Glu	Gly	Phe	Phe	Arg
			340					345					350		
Ala	Pro	Gln	Asp	Pro	Ala	Ser	Met	Pro	Cys	Thr	Arg	Pro	Pro	Ser	Ala
		355					360					365			
Pro	His	Tyr	Leu	Thr	Ala	Val	Gly	Met	Gly	Ala	Lys	Val	Glu	Leu	Arg
	370					375					380				
Trp	Thr	Pro	Pro	Gln	Asp	Ser	Gly	Gly	Arg	Glu	Asp	Ile	Val	Tyr	Ser
385					390					395					400
Val	Thr	Cys	Glu	Gln	Cys	Trp	Pro	Glu	Ser	Gly	Glu	Cys	Gly	Pro	Cys
				405					410					415	
Glu	Ala	Ser	Val	Arg	Tyr	Ser	Glu	Pro	Pro	His	Gly	Leu	Thr	Arg	Thr
			420					425					430		
Ser	Val	Thr	Val	Ser	Asp	Leu	Glu	Pro	His	Met	Asn	Tyr	Thr	Phe	Thr
		435				440					445				
Val	Glu	Ala	Arg	Asn	Gly	Val	Ser	Gly	Leu	Val	Thr	Ser	Arg	Ser	Phe
	450					455					460				
Arg	Thr	Ala	Ser	Val	Ser	Ile	Asn	Gln	Thr	Glu	Pro	Pro	Lys	Val	Arg
465					470					475					480
Leu	Glu	Gly	Arg	Ser	Thr	Thr	Ser	Leu	Ser	Val	Ser	Trp	Ser	Ile	Pro
				485					490					495	

Pro Pro Gln Gln Ser Arg Val Trp Lys Tyr Glu Val Thr Tyr Arg Lys  
500 505 510

Lys Gly Asp Ser Asn Ser Tyr Asn Val Arg Arg Thr Glu Gly Phe Ser  
515 520 525

Val Thr Leu Asp Asp Leu Ala Pro Asp Thr Thr Tyr Leu Val Gln Val  
530 535 540

Gln Ala Leu Thr Gln Glu Gly Gln Gly Ala Gly Ser Arg Val His Glu  
545 550 555 560

Phe Gln Thr

<210> 26  
<211> 1989  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Fusion protein construct

<400> 26  
ggtacctcct ttgattagta tttcctatc tttaaagtac ttttatgtgg aggcattaac 60  
atttggttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata 120  
atattgcgtt tcatctttag aagcgaattt cgccaatatt ataattatca aaagagaggg 180  
gtggcacaacg gtatttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg 240  
aaaaaaataa tgctagtttt tattacactt atattagtta gtctaccaat tgcgcaacaa 300  
actgaagcaa aggatgcatc tgcattcaat aaagaaaatt caatttcac ccatggcacca 360  
ccagcatctc cgccctgcaag tcctaagacg ccaatcgaaa agaaacacgc ggatggatcc 420  
gattataaag atgatgatga taaacaaggt aaagaagttg ttttattaga ttttcagca 480  
gcaggtggtg aattaggttg gttaacacat ccatatggta aaggttgga tttaatgcaa 540  
aatattatga atgatatgcc aatttatatg tatagtgttt gtaatgttat gagtggatgat 600  
caagataaatt gggtacgtac aaattgggtt tatcgtggtg aagcagaacg tttttttatt 660  
gaattaaaat ttacagttcg tgattgtaat agttttccag gtggtgcaag tagttgtaaa 720  
gaaacattta atttatatta tgcagaaagt gatttagatt atggtacaaa ttttcaaaaa 780  
cgtttattta caaaaattga tacaattgca ccagatgaaa ttacagttag tagtgatttt 840  
gaagcacgtc atgttaaatt aaatgttgaa gaacgtagtg ttggtccatt aacacgtaaa 900  
ggtttttatt tagcatttca agatattggg gcatgtgttg cattattaag tgttcgtggt 960  
tattataaaa aatgtccaga attattacaa ggttttagcac attttccaga aacaattgca 1020  
ggtagtgatg caccaagttt agcaacagtt gcaggtacat gtgttgatca tgcagttggt 1080



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ccaccagggtg gtgaagaacc acgtatgcat tgtgcagttg atggtgaatg gttagttcca 1140
attggtcaat gtttatgtca agcaggttat gaaaaagttg aagatgcatg tcaagcatgt 1200
agtccagggtt tttttaaatt tgaagcaagt gaaagtccat gtttagaatg tccagaacat 1260
acattaccaa gtccagaagg tgcaacaagt tgtgaatgtg aagaaggttt ttttcgtgca 1320
ccacaagatc cagcaagtat gccatgtaca cgtccaccaa gtgcaccaca ttatttaaca 1380
gcagttggta tgggtgcaaa agttgaatta cgttggacac caccacaaga tagtgggtggt 1440
cgtgaagata ttgtttatag tgttacatgt gaacaatgtt ggccagaaag tgggtgaatgt 1500
gggccatgtg aagcaagtgt tcgttatagt gaaccaccac atgggtttaac acgtacaagt 1560
gttacagtta gtgatttaga accacatatg aattatacat ttacagttga agcacgtaat 1620
gggtgttagtg gtttagttac aagtcgtagt tttcgtacag caagtgttag tattaatcaa 1680
acagaaccac caaaagttcg tttagaaggt cgtagtacaa caagtttaag tgtagttgg 1740
agtattccac caccacaaca aagtcgtgtt tggaaatatg aagttacata tcgtaaaaaa 1800
ggtgatagta atagttataa tgttcgtcgt acagaagggt ttagtgttac attagatgat 1860
ttagcaccag atacaacata tttagttcaa gttcaagcat taacacaaga aggtcaagggt 1920
gcaggtagtc gtgttcatga atttcaaaca gaacaaaaat taattagtga agaagattta 1980
tgagagctc

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<210> 27

<211> 581

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Predicted fusion protein

<400> 27

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Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
1           5           10           15

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Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
20           25           30

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Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser
35           40           45

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Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Gly Ser Asp Tyr Lys
50           55           60

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Asp Asp Asp Asp Lys Gln Gly Lys Glu Val Val Leu Leu Asp Phe Ala
65           70           75           80

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Ala Ala Gly Gly Glu Leu Gly Trp Leu Thr His Pro Tyr Gly Lys Gly
85           90           95

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Trp	Asp	Leu	Met	Gln	Asn	Ile	Met	Asn	Asp	Met	Pro	Ile	Tyr	Met	Tyr	100	105	110
Ser	Val	Cys	Asn	Val	Met	Ser	Gly	Asp	Gln	Asp	Asn	Trp	Leu	Arg	Thr	115	120	125
Asn	Trp	Val	Tyr	Arg	Gly	Glu	Ala	Glu	Arg	Ile	Phe	Ile	Glu	Leu	Lys	130	135	140
Phe	Thr	Val	Arg	Asp	Cys	Asn	Ser	Phe	Pro	Gly	Gly	Ala	Ser	Ser	Cys	145	150	155
Lys	Glu	Thr	Phe	Asn	Leu	Tyr	Tyr	Ala	Glu	Ser	Asp	Leu	Asp	Tyr	Gly	165	170	175
Thr	Asn	Phe	Gln	Lys	Arg	Leu	Phe	Thr	Lys	Ile	Asp	Thr	Ile	Ala	Pro	180	185	190
Asp	Glu	Ile	Thr	Val	Ser	Ser	Asp	Phe	Glu	Ala	Arg	His	Val	Lys	Leu	195	200	205
Asn	Val	Glu	Glu	Arg	Ser	Val	Gly	Pro	Leu	Thr	Arg	Lys	Gly	Phe	Tyr	210	215	220
Leu	Ala	Phe	Gln	Asp	Ile	Gly	Ala	Cys	Val	Ala	Leu	Leu	Ser	Val	Arg	225	230	235
Val	Tyr	Tyr	Lys	Lys	Cys	Pro	Glu	Leu	Leu	Gln	Gly	Leu	Ala	His	Phe	245	250	255
Pro	Glu	Thr	Ile	Ala	Gly	Ser	Asp	Ala	Pro	Ser	Leu	Ala	Thr	Val	Ala	260	265	270
Gly	Thr	Cys	Val	Asp	His	Ala	Val	Val	Pro	Pro	Gly	Gly	Glu	Glu	Pro	275	280	285
Arg	Met	His	Cys	Ala	Val	Asp	Gly	Glu	Trp	Leu	Val	Pro	Ile	Gly	Gln	290	295	300
Cys	Leu	Cys	Gln	Ala	Gly	Tyr	Glu	Lys	Val	Glu	Asp	Ala	Cys	Gln	Ala	305	310	315
Cys	Ser	Pro	Gly	Phe	Phe	Lys	Phe	Glu	Ala	Ser	Glu	Ser	Pro	Cys	Leu	325	330	335
Glu	Cys	Pro	Glu	His	Thr	Leu	Pro	Ser	Pro	Glu	Gly	Ala	Thr	Ser	Cys	340	345	350
Glu	Cys	Glu	Glu	Gly	Phe	Phe	Arg	Ala	Pro	Gln	Asp	Pro	Ala	Ser	Met	355	360	365
Pro	Cys	Thr	Arg	Pro	Pro	Ser	Ala	Pro	His	Tyr	Leu	Thr	Ala	Val	Gly	370	375	380
Met	Gly	Ala	Lys	Val	Glu	Leu	Arg	Trp	Thr	Pro	Pro	Gln	Asp	Ser	Gly	385	390	395
Gly	Arg	Glu	Asp	Ile	Val	Tyr	Ser	Val	Thr	Cys	Glu	Gln	Cys	Trp	Pro	405	410	415

Glu Ser Gly Glu Cys Gly Pro Cys Glu Ala Ser Val Arg Tyr Ser Glu  
                   420                                  425                                  430  
 Pro Pro His Gly Leu Thr Arg Thr Ser Val Thr Val Ser Asp Leu Glu  
                   435                                  440                                  445  
 Pro His Met Asn Tyr Thr Phe Thr Val Glu Ala Arg Asn Gly Val Ser  
                   450                                  455                                  460  
 Gly Leu Val Thr Ser Arg Ser Phe Arg Thr Ala Ser Val Ser Ile Asn  
                   465                                  470                                  475                                  480  
 Gln Thr Glu Pro Pro Lys Val Arg Leu Glu Gly Arg Ser Thr Thr Ser  
                                   485                                  490                                  495  
 Leu Ser Val Ser Trp Ser Ile Pro Pro Pro Gln Gln Ser Arg Val Trp  
                   500                                  505                                  510  
 Lys Tyr Glu Val Thr Tyr Arg Lys Lys Gly Asp Ser Asn Ser Tyr Asn  
                   515                                  520                                  525  
 Val Arg Arg Thr Glu Gly Phe Ser Val Thr Leu Asp Asp Leu Ala Pro  
                   530                                  535                                  540  
 Asp Thr Thr Tyr Leu Val Gln Val Gln Ala Leu Thr Gln Glu Gly Gln  
                   545                                  550                                  555                                  560  
 Gly Ala Gly Ser Arg Val His Glu Phe Gln Thr Glu Gln Lys Leu Ile  
                                   565                                  570                                  575  
 Ser Glu Glu Asp Leu  
                   580

<210> 28  
 <211> 1989  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Construct for fusion protein

<400> 28  
 ggtacctcct ttgattagta tttcctatc ttaaagttac ttttatgtgg aggcattaac 60  
 atttggttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata 120  
 atattgcggtt tcatcttttag aagcgaattt cgccaatatt ataattatca aaagagaggg 180  
 gtggc aaacg gtatttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg 240  
 aaaaaaatta tgtagtttt tattacatta attttagtta gtttaccaat tgcacaacaa 300  
 acagaagcaa aagatgcaag tgcatttaat aaagaaaata gtattagtag tatggcacca 360  
 ccagcaagtc caccagcaag tccaaaaaca ccaattgaaa aaaaacatgc agatggatcc 420  
 gattataaag atgatgatga taaacaaggt aaagaagttg ttttattaga ttttgcagca 480  
 gcaggtggtg aattaggttg gttaacacat ccatatggta aaggttggga tttaatgcaa 540

aatattatga atgatatgcc aatttatatg tatagtgttt gtaatgttat gagtggatgat	600
caagataaatt gggtacgtac aaattggggtt tatcgtgggtg aagcagaacg tattttttatt	660
gaattaaaaat ttacagttcg tgattgtaat agttttccag gtggtgcaag tagttgtaaa	720
gaaacattta atttatatta tgcagaaagt gatttagatt atggtacaaa ttttcaaaaa	780
cgtttattta caaaaattga tacaattgca ccagatgaaa ttacagttag tagtgatttt	840
gaagcacgtc atgttaaatt aaatgttgaa gaacgtagtg ttggtccatt aacacgtaaa	900
ggtttttatt tagcatttca agatattggg gcatgtgttg cattattaag tgttcgtgtt	960
tattataaaa aatgtccaga attattacaa ggtttagcac attttccaga aacaattgca	1020
ggtagtgatg caccaagttt agcaacagtt gcaggtacat gtgttgatca tgcagttgtt	1080
ccaccaggtg gtgaagaacc acgtatgcat tgtgcagttg atggtgaatg gttagttcca	1140
attggtcaat gtttatgtca agcaggttat gaaaaagttg aagatgcatg tcaagcatgt	1200
agtccaggtt tttttaaatt tgaagcaagt gaaagtccat gtttagaatg tccagaacat	1260
acattaccaa gtccagaagg tgcaacaagt tgtgaatgtg aagaaggttt ttttcgtgca	1320
ccacaagatc cagcaagtat gccatgtaca cgtccaccaa gtgcaccaca ttatttaaca	1380
gcagttggta tgggtgcaaa agttgaatta cgttggacac caccacaaga tagtgggtgg	1440
cgtgaagata ttgtttatag tgttacatgt gaacaatgtt ggccagaaag tggatgaatgt	1500
ggtccatgtg aagcaagtgt tcgttatagt gaaccaccac atgggtttaac acgtacaagt	1560
gttacagtta gtgatttaga accacatatg aattatacat ttacagttga agcacgtaat	1620
ggtgttagtg gtttagttac aagtcgtagt tttcgtacag caagtgttag tattaatcaa	1680
acagaaccac caaaagttcg tttagaaggt cgtagtacaa caagtttaag tgtagttgg	1740
agtattccac caccacaaca aagtcgtgtt tggaaatatg aagttacata tcgtaaaaaa	1800
ggtgatagta atagttataa tggtcgtcgt acagaaggtt ttagtgttac attagatgat	1860
ttagcaccag atacaacata tttagttcaa gttcaagcat taacacaaga aggtcaaggt	1920
gcaggtagtc gtgttcatga atttcaaaca gaacaaaaat taattagtga agaagattta	1980
tgagagctc	1989

<210> 29

<211> 581

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Predicted Fusion protein

<400> 29

Met	Lys	Lys	Ile	Met	Leu	Val	Phe	Ile	Thr	Leu	Ile	Leu	Val	Ser	Leu	1	5	10	15
Pro	Ile	Ala	Gln	Gln	Thr	Glu	Ala	Lys	Asp	Ala	Ser	Ala	Phe	Asn	Lys	20	25	30	
Glu	Asn	Ser	Ile	Ser	Ser	Met	Ala	Pro	Pro	Ala	Ser	Pro	Pro	Ala	Ser	35	40	45	
Pro	Lys	Thr	Pro	Ile	Glu	Lys	Lys	His	Ala	Asp	Gly	Ser	Asp	Tyr	Lys	50	55	60	
Asp	Asp	Asp	Asp	Lys	Gln	Gly	Lys	Glu	Val	Val	Leu	Leu	Asp	Phe	Ala	65	70	75	80
Ala	Ala	Gly	Gly	Glu	Leu	Gly	Trp	Leu	Thr	His	Pro	Tyr	Gly	Lys	Gly	85	90	95	
Trp	Asp	Leu	Met	Gln	Asn	Ile	Met	Asn	Asp	Met	Pro	Ile	Tyr	Met	Tyr	100	105	110	
Ser	Val	Cys	Asn	Val	Met	Ser	Gly	Asp	Gln	Asp	Asn	Trp	Leu	Arg	Thr	115	120	125	
Asn	Trp	Val	Tyr	Arg	Gly	Glu	Ala	Glu	Arg	Ile	Phe	Ile	Glu	Leu	Lys	130	135	140	
Phe	Thr	Val	Arg	Asp	Cys	Asn	Ser	Phe	Pro	Gly	Gly	Ala	Ser	Ser	Cys	145	150	155	160
Lys	Glu	Thr	Phe	Asn	Leu	Tyr	Tyr	Ala	Glu	Ser	Asp	Leu	Asp	Tyr	Gly	165	170	175	
Thr	Asn	Phe	Gln	Lys	Arg	Leu	Phe	Thr	Lys	Ile	Asp	Thr	Ile	Ala	Pro	180	185	190	
Asp	Glu	Ile	Thr	Val	Ser	Ser	Asp	Phe	Glu	Ala	Arg	His	Val	Lys	Leu	195	200	205	
Asn	Val	Glu	Glu	Arg	Ser	Val	Gly	Pro	Leu	Thr	Arg	Lys	Gly	Phe	Tyr	210	215	220	
Leu	Ala	Phe	Gln	Asp	Ile	Gly	Ala	Cys	Val	Ala	Leu	Leu	Ser	Val	Arg	225	230	235	240
Val	Tyr	Tyr	Lys	Lys	Cys	Pro	Glu	Leu	Leu	Gln	Gly	Leu	Ala	His	Phe	245	250	255	
Pro	Glu	Thr	Ile	Ala	Gly	Ser	Asp	Ala	Pro	Ser	Leu	Ala	Thr	Val	Ala	260	265	270	
Gly	Thr	Cys	Val	Asp	His	Ala	Val	Val	Pro	Pro	Gly	Gly	Glu	Glu	Pro	275	280	285	
Arg	Met	His	Cys	Ala	Val	Asp	Gly	Glu	Trp	Leu	Val	Pro	Ile	Gly	Gln	290	295	300	
Cys	Leu	Cys	Gln	Ala	Gly	Tyr	Glu	Lys	Val	Glu	Asp	Ala	Cys	Gln	Ala	305	310	315	320
Cys	Ser	Pro	Gly	Phe	Phe	Lys	Phe	Glu	Ala	Ser	Glu	Ser	Pro	Cys	Leu				

325										330					335				
Glu	Cys	Pro	Glu	His	Thr	Leu	Pro	Ser	Pro	Glu	Gly	Ala	Thr	Ser	Cys				
			340					345					350						
Glu	Cys	Glu	Glu	Gly	Phe	Phe	Arg	Ala	Pro	Gln	Asp	Pro	Ala	Ser	Met				
		355					360					365							
Pro	Cys	Thr	Arg	Pro	Pro	Ser	Ala	Pro	His	Tyr	Leu	Thr	Ala	Val	Gly				
	370					375					380								
Met	Gly	Ala	Lys	Val	Glu	Leu	Arg	Trp	Thr	Pro	Pro	Gln	Asp	Ser	Gly				
385					390					395					400				
Gly	Arg	Glu	Asp	Ile	Val	Tyr	Ser	Val	Thr	Cys	Glu	Gln	Cys	Trp	Pro				
				405					410					415					
Glu	Ser	Gly	Glu	Cys	Gly	Pro	Cys	Glu	Ala	Ser	Val	Arg	Tyr	Ser	Glu				
			420					425					430						
Pro	Pro	His	Gly	Leu	Thr	Arg	Thr	Ser	Val	Thr	Val	Ser	Asp	Leu	Glu				
		435					440					445							
Pro	His	Met	Asn	Tyr	Thr	Phe	Thr	Val	Glu	Ala	Arg	Asn	Gly	Val	Ser				
		450				455					460								
Gly	Leu	Val	Thr	Ser	Arg	Ser	Phe	Arg	Thr	Ala	Ser	Val	Ser	Ile	Asn				
465					470					475					480				
Gln	Thr	Glu	Pro	Pro	Lys	Val	Arg	Leu	Glu	Gly	Arg	Ser	Thr	Thr	Ser				
			485						490					495					
Leu	Ser	Val	Ser	Trp	Ser	Ile	Pro	Pro	Pro	Gln	Gln	Ser	Arg	Val	Trp				
		500					505						510						
Lys	Tyr	Glu	Val	Thr	Tyr	Arg	Lys	Lys	Gly	Asp	Ser	Asn	Ser	Tyr	Asn				
	515						520					525							
Val	Arg	Arg	Thr	Glu	Gly	Phe	Ser	Val	Thr	Leu	Asp	Asp	Leu	Ala	Pro				
	530					535					540								
Asp	Thr	Thr	Tyr	Leu	Val	Gln	Val	Gln	Ala	Leu	Thr	Gln	Glu	Gly	Gln				
545				550						555					560				
Gly	Ala	Gly	Ser	Arg	Val	His	Glu	Phe	Gln	Thr	Glu	Gln	Lys	Leu	Ile				
			565						570					575					
Ser	Glu	Glu	Asp	Leu															
			580																

<210> 30

<211> 1968

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion protein construct

<400> 30

ggtacctcct ttgattagta tattcctatc ttaaagttac ttttatgtgg aggcattaac

60

atttggttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata	120
atattgcggt tcatcttttag aagcgaattt cgccaatatt ataattatca aaagagaggg	180
gtggc aaacg gtatttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg	240
gcatacgaca gtcgttttga tgaatgggta cagaaactga aagaggaaaag ctttcaaaac	300
aatacgtttg accgccgcaa atttattcaa ggagcgggga agattgcagg actttctctt	360
ggattaacga ttgccagtc ggttggggcc tttggatccg attataaaga tgatgatgat	420
aaacaaggta aagaagttgt tttattagat tttgcagcag caggtggtga attaggttgg	480
ttaacacatc catatggtaa aggttgggat ttaatgcaa atattatgaa tgatatgcca	540
atttatatgt atagtgtttg taatgttatg agtggatgac aagataattg gttacgtaca	600
aattgggttt atcgtggtga agcagaacgt atttttattg aattaaaatt tacagttcgt	660
gattgtaata gttttccagg tggtgcaagt agttgtaaag aaacatttaa tttatattat	720
gcagaaagtg atttagatta tggtaaaaat tttcaaaaac gtttatttac aaaaattgat	780
acaattgcac cagatgaaat tacagttagt agtgattttg aagcacgtca tgtaaatta	840
aatgttgaag aacgtagtgt tgggccatta acacgtaaag gtttttattt agcatttcaa	900
gatattggtg catgtgttgc attattaagt gttcgtgttt attataaaaa atgtccagaa	960
ttattacaag gtttagcaca ttttccagaa acaattgcag gtagtgatgc accaagttaa	1020
gcaacagttg caggtacatg tggtgatcat gcagttgttc caccaggtgg tgaagaacca	1080
cgtatgcatt gtgcagttga tggatgaatg ttagttccaa ttggtcaatg tttatgtcaa	1140
gcaggttatg aaaaagttga agatgcatgt caagcatgta gtccaggttt ttttaaattt	1200
gaagcaagtg aaagtccatg tttagaatgt ccagaacata cattaccaag tccagaaggt	1260
gcaacaagtt gtgaatgtga agaaggtttt tttcgtgcac cacaagatcc agcaagtatg	1320
ccatgtacac gtccaccaag tgcaccacat tatttaacag cagttggtat gggtgcaaaa	1380
gttgaattac gttggacacc accacaagat agtgggtggtc gtgaagatat tgtttatagt	1440
gttacatgtg aacaatgttg gccagaaagt ggtgaatgtg gtccatgtga agcaagtgtt	1500
cgttatagtg aaccaccaca tggtttaaca cgtacaagtg ttacagttag tgatttagaa	1560
ccacatatga attatacatt tacagttgaa gcacgtaatg gtgttagtgg tttagttaca	1620
agtcgtagtt ttcgtacagc aagtgttagt attaatacaa cagaaccacc aaaagttcgt	1680
ttagaaggtc gtagtacaac aagtttaagt gttagttgga gtattccacc accacaacaa	1740
agtcgtgttt ggaaatatga agttacatat cgtaaaaaag gtgatagtaa tagttataat	1800
gttcgtcgta cagaaggttt tagtgttaca ttagatgatt tagcaccaga tacaacatat	1860

ttagttcaag	ttcaagcatt	aacacaagaa	ggccaaggtg	caggtagtcg	tgttcatgaa	1920
tttcaaacag	aacaaaaatt	aattagtqaa	gaagatttat	gagagctc		1968



Glu Leu Leu Gln Gly Leu Ala His Phe Pro Glu Thr Ile Ala Gly Ser  
 245 250 255  
 Asp Ala Pro Ser Leu Ala Thr Val Ala Gly Thr Cys Val Asp His Ala  
 260 265 270  
 Val Val Pro Pro Gly Gly Glu Glu Pro Arg Met His Cys Ala Val Asp  
 275 280 285  
 Gly Glu Trp Leu Val Pro Ile Gly Gln Cys Leu Cys Gln Ala Gly Tyr  
 290 295 300  
 Glu Lys Val Glu Asp Ala Cys Gln Ala Cys Ser Pro Gly Phe Phe Lys  
 305 310 315 320  
 Phe Glu Ala Ser Glu Ser Pro Cys Leu Glu Cys Pro Glu His Thr Leu  
 325 330 335  
 Pro Ser Pro Glu Gly Ala Thr Ser Cys Glu Cys Glu Glu Gly Phe Phe  
 340 345 350  
 Arg Ala Pro Gln Asp Pro Ala Ser Met Pro Cys Thr Arg Pro Pro Ser  
 355 360 365  
 Ala Pro His Tyr Leu Thr Ala Val Gly Met Gly Ala Lys Val Glu Leu  
 370 375 380  
 Arg Trp Thr Pro Pro Gln Asp Ser Gly Gly Arg Glu Asp Ile Val Tyr  
 385 390 395 400  
 Ser Val Thr Cys Glu Gln Cys Trp Pro Glu Ser Gly Glu Cys Gly Pro  
 405 410 415  
 Cys Glu Ala Ser Val Arg Tyr Ser Glu Pro Pro His Gly Leu Thr Arg  
 420 425 430  
 Thr Ser Val Thr Val Ser Asp Leu Glu Pro His Met Asn Tyr Thr Phe  
 435 440 445  
 Thr Val Glu Ala Arg Asn Gly Val Ser Gly Leu Val Thr Ser Arg Ser  
 450 455 460  
 Phe Arg Thr Ala Ser Val Ser Ile Asn Gln Thr Glu Pro Pro Lys Val  
 465 470 475 480  
 Arg Leu Glu Gly Arg Ser Thr Thr Ser Leu Ser Val Ser Trp Ser Ile  
 485 490 495  
 Pro Pro Pro Gln Gln Ser Arg Val Trp Lys Tyr Glu Val Thr Tyr Arg  
 500 505 510  
 Lys Lys Gly Asp Ser Asn Ser Tyr Asn Val Arg Arg Thr Glu Gly Phe  
 515 520 525  
 Ser Val Thr Leu Asp Asp Leu Ala Pro Asp Thr Thr Tyr Leu Val Gln  
 530 535 540  
 Val Gln Ala Leu Thr Gln Glu Gly Gln Gly Ala Gly Ser Arg Val His  
 545 550 555 560  
 Glu Phe Gln Thr Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu

565

570

<210> 32  
 <211> 1254  
 <212> DNA  
 <213> Homo sapiens

<400> 32  
 caccgcagga ggaagaacca gcgtgcccgc cagtccccgg aggacgttta cttctccaag 60  
 tcagaacaac tgaagcccct gaagacatac gtggaccccc acacatatga ggaccccaac 120  
 caggctgtgt tgaagtccac taccgagatc catccatcct gtgtcactcg gcagaaggtg 180  
 atcggagcag gagagtttgg ggaggtgtac aagggcatgc tgaagacatc ctcggggaag 240  
 aaggaggtgc cgttgcccat caagacgctg aaagccggct acacagagaa gcagcgagtg 300  
 gacttcctcg gcgaggccgg catcatgggc cagttcagcc accacaacat catccgccta 360  
 gagggcgtca tctccaaata caagcccatg atgatcatca ctgagtacat ggagaatggg 420  
 gccctggaca agttccttcg ggagaaggat ggcgagttca gcgtgctgca gctggtgggc 480  
 atgctgcggg gcatcgcagc tggcatgaag tacctggcca acatgaacta tgtgcaccgt 540  
 gacctggctg cccgcaacat cctcgtcaac agcaacctgg tctgcaagggt gtctgacttt 600  
 ggctgtccc gcgtgctgga ggacgacccc gagggcacct acaccaccag tggcggcaag 660  
 atccccatcc gctggaccgc cccggaggcc atttctacc ggaagtccac ctctgccagc 720  
 gacgtgtgga gctttggcat tgtcatgtgg gaggtgatga cctatggcga gcggccctac 780  
 tgggagttgt ccaaccacga ggtgatgaaa gccatcaatg atggcttccg gctccccaca 840  
 cccatggact gccctccgc catctaccag ctcatgatgc agtgctggca gcaggagcgt 900  
 gcccgcggcc ccaagttcgc tgacatcgtc agcatcctgg acaagctcat tcgtgcccct 960  
 gactccctca agaccctggc tgactttgac ccccgctgtg ctatccggct cccagcacg 1020  
 agcggtcgg agggggtgcc cttccgcacg gtgtccgagt ggctggagtc catcaagatg 1080  
 cagcagtata cggagcactt catggcggcc ggctacactg ccatcgagaa ggtggtgcag 1140  
 atgaccaacg acgacatcaa gaggattggg gtgcggctgc ccggccacca gaagcgcac 1200  
 gcctacagcc tgctgggact caaggaccag gtgaacactg tggggatccc catc 1254

<210> 33  
 <211> 1254  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Sequence Optimized for codon usage in Listeria

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<400> 33
cacagacgta gaaaaaatca acgtgctcga caatccccag aagatgtgta tttttcgaaa      60
agtgaacaat taaaaccatt aaaaacttat gttgatccgc atacgtacga agacccaaat      120
caagcagtat taaaattttac aacagaaaata caccgaagtt gtgtttacaag acaaaaagtt      180
attggagcag gtgaattcgg agaggtatat aaaggtatgt taaaaacatc atcaggtaaa      240
aaagaagttc cggttgcaat taaaacctta aaggcaggat atacagaaaa acagcgagtt      300
gatttttttag gtgaagcagg aattatgggt caatttagcc atcataatat tattcgtttg      360
gaaggagtaa taagtaaata taaaccaatg atgattatta cagaatacat ggaaaacggt      420
gcttttagata aattttttacg tgaaaaggat ggtgaattta gtgtttttaca attggttggt      480
atgttaagag gaattgctgc aggtatgaaa tatttagcta atatgaatta tgttcaccgt      540
gatttggcag caagaaatat cctagtcaat tccaatttag tatgtaaagt tagtgatttt      600
ggtttaagca gagtattaga agacgatcca gaggcaacct atacaacatc gggaggtaaa      660
attcctattc gttggacagc accagaagct atcagttacc gttaaatttac aagtgcacat      720
gacgtgtgga gttttgggat tgtaatgtgg gaagttatga catatggaga aagaccatat      780
tggaattaa gtaatcatga agttatgaaa gcaattaacg atggatttag attaccaact      840
ccgatggatt gtccatctgc catttatcaa ctaatgatgc aatgttggca acaagaaaga      900
gcacgacgtc caaaatttgc agatattggt agtatttttag acaaattaat tcgtgcacca      960
gatagtttaa aaacttttagc agactttgat cctcgtgtta gtattcgatt accaagtacg     1020
tcaggttccg aaggagttcc atttcgcaca gtctccgaat ggttggaatc aattaaatg     1080
caacaatata ccgaacactt tatggcagca ggttacacag caatcgaaaa agttgttcaa     1140
atgacaaatg atgatattaa acgtattgga gttagattac caggccacca gaaacgtatt     1200
gcatattcct tatttaggttt aaaagatcaa gttaataccg tgggaattcc aatt          1254

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<210> 34
<211> 456
<212> PRT
<213> Homo sapiens

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<400> 34

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Val His Glu Phe Gln Thr Leu Ser Pro Glu Gly Ser Gly Asn Leu Ala
1           5           10          15

Val Ile Gly Gly Val Ala Val Gly Val Val Leu Leu Leu Val Leu Ala
20          25          30

Gly Val Gly Phe Phe Ile His Arg Arg Arg Lys Asn Gln Arg Ala Arg
35          40          45

Gln Ser Pro Glu Asp Val Tyr Phe Ser Lys Ser Glu Gln Leu Lys Pro

```

50					55					60					
Leu	Lys	Thr	Tyr	Val	Asp	Pro	His	Thr	Tyr	Glu	Asp	Pro	Asn	Gln	Ala
65					70					75					80
Val	Leu	Lys	Phe	Thr	Thr	Glu	Ile	His	Pro	Ser	Cys	Val	Thr	Arg	Gln
				85					90					95	
Lys	Val	Ile	Gly	Ala	Gly	Glu	Phe	Gly	Glu	Val	Tyr	Lys	Gly	Met	Leu
			100					105					110		
Lys	Thr	Ser	Ser	Gly	Lys	Lys	Glu	Val	Pro	Val	Ala	Ile	Lys	Thr	Leu
		115					120					125			
Lys	Ala	Gly	Tyr	Thr	Glu	Lys	Gln	Arg	Val	Asp	Phe	Leu	Gly	Glu	Ala
	130					135					140				
Gly	Ile	Met	Gly	Gln	Phe	Ser	His	His	Asn	Ile	Ile	Arg	Leu	Glu	Gly
145					150				155					160	
Val	Ile	Ser	Lys	Tyr	Lys	Pro	Met	Met	Ile	Ile	Thr	Glu	Tyr	Met	Glu
				165					170					175	
Asn	Gly	Ala	Leu	Asp	Lys	Phe	Leu	Arg	Glu	Lys	Asp	Gly	Glu	Phe	Ser
			180					185					190		
Val	Leu	Gln	Leu	Val	Gly	Met	Leu	Arg	Gly	Ile	Ala	Ala	Gly	Met	Lys
		195					200					205			
Tyr	Leu	Ala	Asn	Met	Asn	Tyr	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn
	210					215					220				
Ile	Leu	Val	Asn	Ser	Asn	Leu	Val	Cys	Lys	Val	Ser	Asp	Phe	Gly	Leu
225						230					235				240
Ser	Arg	Val	Leu	Glu	Asp	Asp	Pro	Glu	Ala	Thr	Tyr	Thr	Thr	Ser	Gly
				245					250					255	
Gly	Lys	Ile	Pro	Ile	Arg	Trp	Thr	Ala	Pro	Glu	Ala	Ile	Ser	Tyr	Arg
			260					265					270		
Lys	Phe	Thr	Ser	Ala	Ser	Asp	Val	Trp	Ser	Phe	Gly	Ile	Val	Met	Trp
		275					280					285			
Glu	Val	Met	Thr	Tyr	Gly	Glu	Arg	Pro	Tyr	Trp	Glu	Leu	Ser	Asn	His
	290					295					300				
Glu	Val	Met	Lys	Ala	Ile	Asn	Asp	Gly	Phe	Arg	Leu	Pro	Thr	Pro	Met
305					310					315					320
Asp	Cys	Pro	Ser	Ala	Ile	Tyr	Gln	Leu	Met	Met	Gln	Cys	Trp	Gln	Gln
				325					330					335	
Glu	Arg	Ala	Arg	Arg	Pro	Lys	Phe	Ala	Asp	Ile	Val	Ser	Ile	Leu	Asp
			340					345					350		
Lys	Leu	Ile	Arg	Ala	Pro	Asp	Ser	Leu	Lys	Thr	Leu	Ala	Asp	Phe	Asp
		355					360					365			
Pro	Arg	Val	Ser	Ile	Arg	Leu	Pro	Ser	Thr	Ser	Gly	Ser	Glu	Gly	Val
	370					375					380				

Pro Phe Arg Thr Val Ser Glu Trp Leu Glu Ser Ile Lys Met Gln Gln  
 385 390 395 400

Tyr Thr Glu His Phe Met Ala Ala Gly Tyr Thr Ala Ile Glu Lys Val  
 405 410 415

Val Gln Met Thr Asn Asp Asp Ile Lys Arg Ile Gly Val Arg Leu Pro  
 420 425 430

Gly His Gln Lys Arg Ile Ala Tyr Ser Leu Leu Gly Leu Lys Asp Gln  
 435 440 445

Val Asn Thr Val Gly Ile Pro Ile  
 450 455

<210> 35  
 <211> 1437  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion Protein

<400> 35  
 atgaaaaaaa taatgctagt ttttattaca cttatattag ttagtctacc aattgcgcaa 60  
 caaactgaag caaaggatgc atctgcattc aataaagaaa attcaatttc atccatggca 120  
 ccaccagcat ctccgcctgc aagtcctaag acgccaatcg aaaagaaaca cgcggatctc 180  
 gagcaccgca ggaggaagaa ccagcgtgcc cgccagtccc cggaggacgt ttacttctcc 240  
 aagtcagaac aactgaagcc cctgaagaca tacgtggacc cccacacata tgaggacccc 300  
 aaccaggctg tgttgaagtt cactaccgag atccatccat cctgtgtcac tcggcagaag 360  
 gtgatcggag caggagagtt tggggaggtg tacaagggca tgctgaagac atcctcgggg 420  
 aagaaggagg tgccggtggc catcaagacg ctgaaagccg gctacacaga gaagcagcga 480  
 gtggacttcc tcggcgaggc cggcatcatg ggccagttca gccaccacaa catcatccgc 540  
 ctagagggcg tcatctccaa atacaagccc atgatgatca tcaactgagta catggagaat 600  
 ggggccctgg acaagttcct tcgggagaag gatggcgagt tcagcgtgct gcagctggtg 660  
 ggcattgctgc ggggcatcgc agctggcatg aagtacctgg ccaacatgaa ctatgtgcac 720  
 cgtgacctgg ctgcccgcaa catcctcgtc aacagcaacc tgggtctgcaa ggtgtctgac 780  
 tttggcctgt cccgcgtgct ggaggacgac cccgaggcca cctacaccac cagtggcggc 840  
 aagatcccca tccgctggac cgccccggag gccatttcct accggaagtt cacctctgcc 900  
 agcgacgtgt ggagcttttg cattgtcatg tgggaggtga tgacctatgg cgagcggccc 960  
 tactgggagt tgtccaacca cgaggtgatg aaagccatca atgatggctt ccggctcccc 1020  
 acacccatgg actgcccctc cgccatctac cagctcatga tgcagtgtg gcagcaggag 1080

cgtgcccgcc gccccaagtt cgctgacatc gtcagcatcc tggacaagct cattcgtgcc 1140  
 cctgactccc tcaagaccct ggctgacttt gacccccgcg tgtctatccg gctccccagc 1200  
 acgagcgggt cggaggggggt gcccttccgc acggtgtccg agtgggtgga gtccatcaag 1260  
 atgcagcagt atacggagca cttcatggcg gccggctaca ctgccatcga gaaggtggtg 1320  
 cagatgacca acgacgacat caagaggatt ggggtgcggc tgccccggcca ccagaagcgc 1380  
 atcgctaca gcctgctggg actcaaggac caggtgaaca ctgtggggat ccccatc 1437

<210> 36

<211> 479

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Predicted Protein Sequence

<400> 36

Met	Lys	Lys	Ile	Met	Leu	Val	Phe	Ile	Thr	Leu	Ile	Leu	Val	Ser	Leu	1	5	10	15
Pro	Ile	Ala	Gln	Gln	Thr	Glu	Ala	Lys	Asp	Ala	Ser	Ala	Phe	Asn	Lys	20	25	30	
Glu	Asn	Ser	Ile	Ser	Ser	Met	Ala	Pro	Pro	Ala	Ser	Pro	Pro	Ala	Ser	35	40	45	
Pro	Lys	Thr	Pro	Ile	Glu	Lys	Lys	His	Ala	Asp	Leu	Glu	His	Arg	Arg	50	55	60	
Arg	Lys	Asn	Gln	Arg	Ala	Arg	Gln	Ser	Pro	Glu	Asp	Val	Tyr	Phe	Ser	65	70	75	80
Lys	Ser	Glu	Gln	Leu	Lys	Pro	Leu	Lys	Thr	Tyr	Val	Asp	Pro	His	Thr	85	90	95	
Tyr	Glu	Asp	Pro	Asn	Gln	Ala	Val	Leu	Lys	Phe	Thr	Thr	Glu	Ile	His	100	105	110	
Pro	Ser	Cys	Val	Thr	Arg	Gln	Lys	Val	Ile	Gly	Ala	Gly	Glu	Phe	Gly	115	120	125	
Glu	Val	Tyr	Lys	Gly	Met	Leu	Lys	Thr	Ser	Ser	Gly	Lys	Lys	Glu	Val	130	135	140	
Pro	Val	Ala	Ile	Lys	Thr	Leu	Lys	Ala	Gly	Tyr	Thr	Glu	Lys	Gln	Arg	145	150	155	160
Val	Asp	Phe	Leu	Gly	Glu	Ala	Gly	Ile	Met	Gly	Gln	Phe	Ser	His	His	165	170	175	
Asn	Ile	Ile	Arg	Leu	Glu	Gly	Val	Ile	Ser	Lys	Tyr	Lys	Pro	Met	Met	180	185	190	
Ile	Ile	Thr	Glu	Tyr	Met	Glu	Asn	Gly	Ala	Leu	Asp	Lys	Phe	Leu	Arg				

195					200					205					
Glu	Lys	Asp	Gly	Glu	Phe	Ser	Val	Leu	Gln	Leu	Val	Gly	Met	Leu	Arg
210						215					220				
Gly	Ile	Ala	Ala	Gly	Met	Lys	Tyr	Leu	Ala	Asn	Met	Asn	Tyr	Val	His
225					230					235					240
Arg	Asp	Leu	Ala	Ala	Arg	Asn	Ile	Leu	Val	Asn	Ser	Asn	Leu	Val	Cys
				245					250					255	
Lys	Val	Ser	Asp	Phe	Gly	Leu	Ser	Arg	Val	Leu	Glu	Asp	Asp	Pro	Glu
			260					265					270		
Ala	Thr	Tyr	Thr	Thr	Ser	Gly	Gly	Lys	Ile	Pro	Ile	Arg	Trp	Thr	Ala
			275				280					285			
Pro	Glu	Ala	Ile	Ser	Tyr	Arg	Lys	Phe	Thr	Ser	Ala	Ser	Asp	Val	Trp
	290					295					300				
Ser	Phe	Gly	Ile	Val	Met	Trp	Glu	Val	Met	Thr	Tyr	Gly	Glu	Arg	Pro
305					310					315					320
Tyr	Trp	Glu	Leu	Ser	Asn	His	Glu	Val	Met	Lys	Ala	Ile	Asn	Asp	Gly
				325					330					335	
Phe	Arg	Leu	Pro	Thr	Pro	Met	Asp	Cys	Pro	Ser	Ala	Ile	Tyr	Gln	Leu
			340					345					350		
Met	Met	Gln	Cys	Trp	Gln	Gln	Glu	Arg	Ala	Arg	Arg	Pro	Lys	Phe	Ala
		355					360					365			
Asp	Ile	Val	Ser	Ile	Leu	Asp	Lys	Leu	Ile	Arg	Ala	Pro	Asp	Ser	Leu
	370					375					380				
Lys	Thr	Leu	Ala	Asp	Phe	Asp	Pro	Arg	Val	Ser	Ile	Arg	Leu	Pro	Ser
385					390					395					400
Thr	Ser	Gly	Ser	Glu	Gly	Val	Pro	Phe	Arg	Thr	Val	Ser	Glu	Trp	Leu
				405					410					415	
Glu	Ser	Ile	Lys	Met	Gln	Gln	Tyr	Thr	Glu	His	Phe	Met	Ala	Ala	Gly
			420					425					430		
Tyr	Thr	Ala	Ile	Glu	Lys	Val	Val	Gln	Met	Thr	Asn	Asp	Asp	Ile	Lys
		435					440					445			
Arg	Ile	Gly	Val	Arg	Leu	Pro	Gly	His	Gln	Lys	Arg	Ile	Ala	Tyr	Ser
	450					455					460				
Leu	Leu	Gly	Leu	Lys	Asp	Gln	Val	Asn	Thr	Val	Gly	Ile	Pro	Ile	
465					470					475					

<210> 37

<211> 1737

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion protein sequence

<400> 37

ggtacctcct ttgattagta tattcctatc ttaaagttac ttttatgtgg aggcattaac	60
at ttgttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata	120
atattgcggt tcatcttttag aagcgaat tt cgccaatatt ataattatca aaagagaggg	180
gtggcaaacg gtat ttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg	240
aaaaaaataa tgctagtttt tattacactt atattagtta gtctaccaat tgcgcaacaa	300
actgaagcaa aggatgcatc tgcattcaat aaagaaaatt caatttcac catggcacca	360
ccagcatctc cgcctgcaag tcctaagacg ccaatcgaaa agaaacacgc ggatggatcc	420
gattataaag atgatgatga taaacacaga cgtagaaaaa atcaacgtgc tcgacaatcc	480
ccagaagatg tgtat ttttc gaaaagtga caattaaaac cattaataaac ttatgttgat	540
ccgcatacgt acgaagaccc aaatcaagca gtattaaaat ttacaacaga aatacaccca	600
agttgtgtta caagacaaaa agttattgga gcaggtgaat tcggagaggt atataaaggt	660
atgttaaaaa catcatcagg taaaaaagaa gttccggttg caattaaaac cttaaaggca	720
ggatatacag aaaaacacgc agttgatttt ttaggtgaag caggaattat gggatcaattt	780
agccatcata atattattcg tttggaagga gtaataagta aatataaacc aatgatgatt	840
attacagaat acatggaaaa cgggtgcttta gataaatttt tacgtgaaaa ggatggtgaa	900
tttagtgttt tacaattggt tggtatgtta agaggaattg ctgcagggtat gaaatattta	960
gctaatatga attatgttca ccgtgatttg gcagcaagaa ataccctagt caattccaat	1020
ttagtatgta aagttagtga ttttggttta agcagagtat tagaagacga tccagaggca	1080
acctatacaa catcgggagg taaaattcct attcgttgga cagcaccaga agctatcagt	1140
taccgtaaat ttacaagtgc atcagacgtg tggagttttg ggattgtaat gtgggaagtt	1200
atgacatatg gagaaagacc atattgggaa ttaagtaatc atgaagtat gaaagcaatt	1260
aacgatggat ttagattacc aactccgatg gattgtccat ctgccattta tcaactaatg	1320
atgcaatggt ggcaacaaga aagagcacga cgtccaaaat ttgcagatat tgttagtatt	1380
ttagacaaat taattcgtgc accagatagt ttaaaaaact tagcagactt tgatcctcgt	1440
gtagtat ttc gattaccaag tacgtcaggt tccgaaggag ttccatttcg cacagtctcc	1500
gaatggtttg aatcaattaa aatgcaacaa tacaccgaac actttatggc agcaggttac	1560
acagcaatcg aaaaagttgt tcaaatgaca aatgatgata ttaaacgtat tggagttaga	1620
ttaccaggcc accagaaacg tattgcatat tctttattag gtttaaaaga tcaagttaat	1680
accgtgggaa ttccaattga acaaaaatta atttccgaag aagacttata agagctc	1737



<210> 38  
 <211> 497  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Predicted fusion protein  
  
 <400> 38  
  
 Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu  
 1 5 10 15  
 Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys  
 20 25 30  
 Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser  
 35 40 45  
 Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Gly Ser Asp Tyr Lys  
 50 55 60  
 Asp Asp Asp Asp Lys His Arg Arg Arg Lys Asn Gln Arg Ala Arg Gln  
 65 70 75 80  
 Ser Pro Glu Asp Val Tyr Phe Ser Lys Ser Glu Gln Leu Lys Pro Leu  
 85 90 95  
 Lys Thr Tyr Val Asp Pro His Thr Tyr Glu Asp Pro Asn Gln Ala Val  
 100 105 110  
 Leu Lys Phe Thr Thr Glu Ile His Pro Ser Cys Val Thr Arg Gln Lys  
 115 120 125  
 Val Ile Gly Ala Gly Glu Phe Gly Glu Val Tyr Lys Gly Met Leu Lys  
 130 135 140  
 Thr Ser Ser Gly Lys Lys Glu Val Pro Val Ala Ile Lys Thr Leu Lys  
 145 150 155 160  
 Ala Gly Tyr Thr Glu Lys Gln Arg Val Asp Phe Leu Gly Glu Ala Gly  
 165 170 175  
 Ile Met Gly Gln Phe Ser His His Asn Ile Ile Arg Leu Glu Gly Val  
 180 185 190  
 Ile Ser Lys Tyr Lys Pro Met Met Ile Ile Thr Glu Tyr Met Glu Asn  
 195 200 205  
 Gly Ala Leu Asp Lys Phe Leu Arg Glu Lys Asp Gly Glu Phe Ser Val  
 210 215 220  
 Leu Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ala Gly Met Lys Tyr  
 225 230 235 240  
 Leu Ala Asn Met Asn Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile  
 245 250 255  
 Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser  
 260 265 270

Arg Val Leu Glu Asp Asp Pro Glu Ala Thr Tyr Thr Thr Ser Gly Gly  
 275 280 285  
 Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ser Tyr Arg Lys  
 290 295 300  
 Phe Thr Ser Ala Ser Asp Val Trp Ser Phe Gly Ile Val Met Trp Glu  
 305 310 315 320  
 Val Met Thr Tyr Gly Glu Arg Pro Tyr Trp Glu Leu Ser Asn His Glu  
 325 330 335  
 Val Met Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro Thr Pro Met Asp  
 340 345 350  
 Cys Pro Ser Ala Ile Tyr Gln Leu Met Met Gln Cys Trp Gln Gln Glu  
 355 360 365  
 Arg Ala Arg Arg Pro Lys Phe Ala Asp Ile Val Ser Ile Leu Asp Lys  
 370 375 380  
 Leu Ile Arg Ala Pro Asp Ser Leu Lys Thr Leu Ala Asp Phe Asp Pro  
 385 390 395 400  
 Arg Val Ser Ile Arg Leu Pro Ser Thr Ser Gly Ser Glu Gly Val Pro  
 405 410 415  
 Phe Arg Thr Val Ser Glu Trp Leu Glu Ser Ile Lys Met Gln Gln Tyr  
 420 425 430  
 Thr Glu His Phe Met Ala Ala Gly Tyr Thr Ala Ile Glu Lys Val Val  
 435 440 445  
 Gln Met Thr Asn Asp Asp Ile Lys Arg Ile Gly Val Arg Leu Pro Gly  
 450 455 460  
 His Gln Lys Arg Ile Ala Tyr Ser Leu Leu Gly Leu Lys Asp Gln Val  
 465 470 475 480  
 Asn Thr Val Gly Ile Pro Ile Glu Gln Lys Leu Ile Ser Glu Glu Asp  
 485 490 495

Leu

<210> 39

<211> 1737

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion protein construct

<400> 39

ggtagcctcct ttgattagta tattcctatc ttaaagttac ttttatgtgg aggcattaac 60

atttggttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata 120

atattgcggtt tcatcttttag aagcgaattt cgccaatatt ataattatca aaagagaggg 180

gtggcaaacg gtatttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg	240
aaaaaaatta tgtagtttt tattacatta attttagtta gtttaccatg tgcacaacaa	300
acagaagcaa aagatgcaag tgcatttaaat aaagaaaata gtattagtag tatggcacca	360
ccagcaagtc caccagcaag tccaaaaaca ccaattgaaa aaaaacatgc agatggatcc	420
gattataaag acgatgatga taaacacaga cgtagaaaaa atcaacgtgc tcgacaatcc	480
ccagaagatg tgtatttttc gaaaagtga caattaaaac cattaaaaac ttatgttgat	540
ccgcatacgt acgaagaccc aaatcaagca gtattaaaat ttacaacaga aatacaccca	600
agttgtgtta caagacaaaa agttattgga gcaggtgaat tcggagaggt atataaaggt	660
atgttaaaaa catcatcagg taaaaaagaa gttccggttg caattaaaac cttaaaggca	720
ggatatacag aaaaacagcg agttgatttt ttaggtgaag caggaattat gggatcaattt	780
agccatcata atattattcg tttggaagga gtaataagta aatataaacc aatgatgatt	840
attacagaat acatggaaaa cgggtgcttta gataaatttt tacgtgaaaa ggatgggtgaa	900
tttagtggtt tacaattggt tggtagtga agaggaattg ctgcaggtat gaaatattta	960
gctaatatga attatgttca ccgtgatttg gcagcaagaa ataccctagt caattccaat	1020
ttagtatgta aagttagtga ttttggttta agcagagtat tagaagacga tccagaggca	1080
acctatacaa catcggggagg taaaattcct attcgttgga cagcaccaga agctatcagt	1140
taccgtaaat ttacaagtgc atcagacgtg tggagttttg ggattgtaat gtgggaagtt	1200
atgacatatg gagaaagacc atattgggaa ttaagtaatc atgaagttat gaaagcaatt	1260
aacgatggat ttagattacc aactccgatg gattgtccat ctgccattta tcaactaatg	1320
atgcaatggt ggcaacaaga aagagcacga cgtccaaaat ttgcagatat tgtagtatt	1380
ttagacaaat taattcgtgc accagatagt ttaaaaactt tagcagactt tgatcctcgt	1440
gtagtatatt gattaccaag tacgtcaggt tccgaaggag ttccatttcg cacagtctcc	1500
gaatggttgg aatcaattaa aatgcaacaa tacaccgaac actttatggc agcaggttac	1560
acagcaatcg aaaaagttgt tcaaatgaca aatgatgata ttaaactgat tggagttaga	1620
ttaccaggcc accagaaacg tattgcataat tctttattag gtttaaaaga tcaagttaat	1680
accgtgggaa ttccaattga aaaaaatta atttccgaag aagacttata agagctc	1737

<210> 40

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Predicted Fusion Protein

<400> 40

Met	Lys	Lys	Ile	Met	Leu	Val	Phe	Ile	Thr	Leu	Ile	Leu	Val	Ser	Leu	
1				5					10					15		
Pro	Ile	Ala	Gln	Gln	Thr	Glu	Ala	Lys	Asp	Ala	Ser	Ala	Phe	Asn	Lys	
			20					25					30			
Glu	Asn	Ser	Ile	Ser	Ser	Met	Ala	Pro	Pro	Ala	Ser	Pro	Pro	Ala	Ser	
		35					40					45				
Pro	Lys	Thr	Pro	Ile	Glu	Lys	Lys	His	Ala	Asp	Gly	Ser	Asp	Tyr	Lys	
	50					55					60					
Asp	Asp	Asp	Asp	Lys	His	Arg	Arg	Arg	Lys	Asn	Gln	Arg	Ala	Arg	Gln	
5					70					75					80	
Ser	Pro	Glu	Asp	Val	Tyr	Phe	Ser	Lys	Ser	Glu	Gln	Leu	Lys	Pro	Leu	
				85					90					95		
Lys	Thr	Tyr	Val	Asp	Pro	His	Thr	Tyr	Glu	Asp	Pro	Asn	Gln	Ala	Val	
			100					105					110			
Leu	Lys	Phe	Thr	Thr	Glu	Ile	His	Pro	Ser	Cys	Val	Thr	Arg	Gln	Lys	
		115					120						125			
Val	Ile	Gly	Ala	Gly	Glu	Phe	Gly	Glu	Val	Tyr	Lys	Gly	Met	Leu	Lys	
	130					135					140					
Thr	Ser	Ser	Gly	Lys	Lys	Glu	Val	Pro	Val	Ala	Ile	Lys	Thr	Leu	Lys	
145					150					155					160	
Ala	Gly	Tyr	Thr	Glu	Lys	Gln	Arg	Val	Asp	Phe	Leu	Gly	Glu	Ala	Gly	
				165					170					175		
Ile	Met	Gly	Gln	Phe	Ser	His	His	Asn	Ile	Ile	Arg	Leu	Glu	Gly	Val	
			180					185					190			
Ile	Ser	Lys	Tyr	Lys	Pro	Met	Met	Ile	Ile	Thr	Glu	Tyr	Met	Glu	Asn	
		195					200					205				
Gly	Ala	Leu	Asp	Lys	Phe	Leu	Arg	Glu	Lys	Asp	Gly	Glu	Phe	Ser	Val	
	210					215					220					
Leu	Gln	Leu	Val	Gly	Met	Leu	Arg	Gly	Ile	Ala	Ala	Gly	Met	Lys	Tyr	
225					230					235					240	
Leu	Ala	Asn	Met	Asn	Tyr	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Ile	
				245					250					255		
Leu	Val	Asn	Ser	Asn	Leu	Val	Cys	Lys	Val	Ser	Asp	Phe	Gly	Leu	Ser	
			260					265					270			
Arg	Val	Leu	Glu	Asp	Asp	Pro	Glu	Ala	Thr	Tyr	Thr	Thr	Ser	Gly	Gly	
		275					280						285			
Lys	Ile	Pro	Ile	Arg	Trp	Thr	Ala	Pro	Glu	Ala	Ile	Ser	Tyr	Arg	Lys	
	290					295					300					
Phe	Thr	Ser	Ala	Ser	Asp	Val	Trp	Ser	Phe	Gly	Ile	Val	Met	Trp	Glu	
305					310					315					320	

Val Met Thr Tyr Gly Glu Arg Pro Tyr Trp Glu Leu Ser Asn His Glu  
 325 330 335  
 Val Met Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro Thr Pro Met Asp  
 340 345 350  
 Cys Pro Ser Ala Ile Tyr Gln Leu Met Met Gln Cys Trp Gln Gln Glu  
 355 360 365  
 Arg Ala Arg Arg Pro Lys Phe Ala Asp Ile Val Ser Ile Leu Asp Lys  
 370 375 380  
 Leu Ile Arg Ala Pro Asp Ser Leu Lys Thr Leu Ala Asp Phe Asp Pro  
 385 390 395 400  
 Arg Val Ser Ile Arg Leu Pro Ser Thr Ser Gly Ser Glu Gly Val Pro  
 405 410 415  
 Phe Arg Thr Val Ser Glu Trp Leu Glu Ser Ile Lys Met Gln Gln Tyr  
 420 425 430  
 Thr Glu His Phe Met Ala Ala Gly Tyr Thr Ala Ile Glu Lys Val Val  
 435 440 445  
 Gln Met Thr Asn Asp Asp Ile Lys Arg Ile Gly Val Arg Leu Pro Gly  
 450 455 460  
 His Gln Lys Arg Ile Ala Tyr Ser Leu Leu Gly Leu Lys Asp Gln Val  
 465 470 475 480  
 Asn Thr Val Gly Ile Pro Ile Glu Gln Lys Leu Ile Ser Glu Glu Asp  
 485 490 495  
 Leu

<210> 41  
 <211> 1716  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion protein construct

<400> 41  
 ggtacctcct ttgattagta tattcctatc ttaaagttac ttttatgtgg aggcattaac 60  
 atttggttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata 120  
 atattgcggtt tcattcttag aagcgaattt cgccaatatt ataattatca aaagagaggg 180  
 gtggcaaacg gtatttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg 240  
 gcatacgaca gtcgttttga tgaatgggta cagaaactga aagaggaaag ctttcaaaac 300  
 aatacgtttg accgccgcaa atttattcaa ggagcgggga agattgcagg actttctctt 360  
 ggattaacga ttgcccagtc ggttggggcc tttggatccg attataaaga tgatgatgat 420

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aaacacagac gtagaaaaaa tcaacgtgct cgacaatccc cagaagatgt gtatttttcg      480
aaaagtgaac aattaaaacc attaaaaact tatgttgatc cgcatacgta cgaagaccca      540
aatcaagcag tattaaaatt tacaacagaa atacacccaa gttgtgttac aagacaaaaa      600
gttattggag caggtgaatt cggagaggta tataaaggta tgttaaaaac atcatcaggt      660
aaaaaagaag ttccggttgc aattaaaacc ttaaaggcag gatatacaga aaaacagcga      720
gttgattttt taggtgaagc aggaattatg ggtcaattta gccatcataa tattattcgt      780
ttggaaggag taataagtaa atataaacca atgatgatta ttacagaata catggaaaac      840
ggtgcttttag ataaattttt acgtgaaaag gatggtgaat ttagtgtttt acaattggtt      900
ggtatgttaa gaggaattgc tgcaggtatg aaatatttag ctaatatgaa ttatgttcac      960
cgtgatttgg cagcaagaaa taccctagtc aattccaatt tagtatgtaa agttagtgat     1020
tttggtttta gcagagtatt agaagacgat ccagaggcaa cctatacaac atcgggaggt     1080
aaaattccta ttcgttggac agcaccagaa gctatcagtt accgtaaatt tacaagtgca     1140
tcagacgtgt ggagttttgg gattgtaatg tgggaagtta tgacatatgg agaaagacca     1200
tattgggaat taagtaatca tgaagttatg aaagcaatta acgatggatt tagattacca     1260
actccgatgg attgtccatc tgccatttat caactaatga tgcaatgttg gcaacaagaa     1320
agagcacgac gtccaaaatt tgcagatatt gttagtattt tagacaaatt aattcgtgca     1380
ccagatagtt taaaaacttt agcagacttt gatcctcgtg ttagtattcg attaccaagt     1440
acgtcaggtt ccgaaggagt tccatttcgc acagtctcgc aatggttgga atcaattaaa     1500
atgcaacaat acaccgaaca ctttatggca gcaggttaca cagcaatcga aaaagttggt     1560
caaatgacaa atgatgatat taaacgtatt ggagtttagat taccaggcca ccagaaacgt     1620
attgcatatt ctttattagg tttaaaagat caagttaata ccgtgggaat tccaattgaa     1680
caaaaattaa tttccgaaga agacttataa gagctc                                1716

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<210> 42

<211> 490

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Predicted fusion protein

<400> 42

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Met Ala Tyr Asp Ser Arg Phe Asp Glu Trp Val Gln Lys Leu Lys Glu
1           5           10           15

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Glu Ser Phe Gln Asn Asn Thr Phe Asp Arg Arg Lys Phe Ile Gln Gly
20           25           30

```

Ala Gly Lys Ile Ala Gly Leu Ser Leu Gly Leu Thr Ile Ala Gln Ser  
 35 40 45  
 Val Gly Ala Phe Gly Ser Asp Tyr Lys Asp Asp Asp Lys His Arg  
 50 55 60  
 Arg Arg Lys Asn Gln Arg Ala Arg Gln Ser Pro Glu Asp Val Tyr Phe  
 65 70 75 80  
 Ser Lys Ser Glu Gln Leu Lys Pro Leu Lys Thr Tyr Val Asp Pro His  
 85 90 95  
 Thr Tyr Glu Asp Pro Asn Gln Ala Val Leu Lys Phe Thr Thr Glu Ile  
 100 105 110  
 His Pro Ser Cys Val Thr Arg Gln Lys Val Ile Gly Ala Gly Glu Phe  
 115 120 125  
 Gly Glu Val Tyr Lys Gly Met Leu Lys Thr Ser Ser Gly Lys Lys Glu  
 130 135 140  
 Val Pro Val Ala Ile Lys Thr Leu Lys Ala Gly Tyr Thr Glu Lys Gln  
 145 150 155 160  
 Arg Val Asp Phe Leu Gly Glu Ala Gly Ile Met Gly Gln Phe Ser His  
 165 170 175  
 His Asn Ile Ile Arg Leu Glu Gly Val Ile Ser Lys Tyr Lys Pro Met  
 180 185 190  
 Met Ile Ile Thr Glu Tyr Met Glu Asn Gly Ala Leu Asp Lys Phe Leu  
 195 200 205  
 Arg Glu Lys Asp Gly Glu Phe Ser Val Leu Gln Leu Val Gly Met Leu  
 210 215 220  
 Arg Gly Ile Ala Ala Gly Met Lys Tyr Leu Ala Asn Met Asn Tyr Val  
 225 230 235 240  
 His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val  
 245 250 255  
 Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro  
 260 265 270  
 Glu Ala Thr Tyr Thr Thr Ser Gly Gly Lys Ile Pro Ile Arg Trp Thr  
 275 280 285  
 Ala Pro Glu Ala Ile Ser Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val  
 290 295 300  
 Trp Ser Phe Gly Ile Val Met Trp Glu Val Met Thr Tyr Gly Glu Arg  
 305 310 315 320  
 Pro Tyr Trp Glu Leu Ser Asn His Glu Val Met Lys Ala Ile Asn Asp  
 325 330 335  
 Gly Phe Arg Leu Pro Thr Pro Met Asp Cys Pro Ser Ala Ile Tyr Gln  
 340 345 350  
 Leu Met Met Gln Cys Trp Gln Gln Glu Arg Ala Arg Arg Pro Lys Phe

355		360		365
Ala Asp Ile Val Ser Ile Leu Asp Lys Leu Ile Arg Ala Pro Asp Ser				
370		375		380
Leu Lys Thr Leu Ala Asp Phe Asp Pro Arg Val Ser Ile Arg Leu Pro				
385		390		400
Ser Thr Ser Gly Ser Glu Gly Val Pro Phe Arg Thr Val Ser Glu Trp				
	405		410	415
Leu Glu Ser Ile Lys Met Gln Gln Tyr Thr Glu His Phe Met Ala Ala				
	420		425	430
Gly Tyr Thr Ala Ile Glu Lys Val Val Gln Met Thr Asn Asp Asp Ile				
	435		440	445
Lys Arg Ile Gly Val Arg Leu Pro Gly His Gln Lys Arg Ile Ala Tyr				
	450		455	460
Ser Leu Leu Gly Leu Lys Asp Gln Val Asn Thr Val Gly Ile Pro Ile				
465		470		475
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu				
	485		490	

<210> 43

<211> 9808

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion Protein Construct

<400> 43

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ttgatacttg tacaattcaa tgacaaggct attaatcaaa cgccttaaatt tttcatcttc	180
aataccattc attgagggta aatttaagac ttccaggggt gcccccttaa tttgaatttg	240
attcatcaat tctgttaatt ctttattatt tcgtcctaatt cgatctaatt cagtaacaat	300
aacaatatcc ccttcacgaa tatagttaag catagcttgt aattgtgggc gttcgaccga	360
ttgaccgctt aatttgctctg aaaagacctt agaaacgccc tgtaacgctt gtaattgccg	420
atctaagttc tggtctttgc tactgacacg tgcataacca atttttagcca ttttcaacca	480
acctctaaaa ttctctcggt tgcaataacc aatcagcaat atctactttt tcaatttcaa	540
attgcttatac agaaattgtc ttttcgtaag cgataaaatc ttgcgcatat tgttgctcat	600
taaaaatagc caccacttcg tcatttttcta aaactcgata aataaatttt ttcattttac	660
tcctcctatt atgccaact taaatgacct attcaccaag tcaattatac tgctaaaatc	720
atattaggac aaataggtat actctattga cctataaatg atagcaactt aaaagatcaa	780



gtgttcgctt cgctctcact gcccctcgac gttttagtag cctttccctc acttcggttca	840
gtccaagcca actaaaagtt ttcgggctac tctctccttc tccccctaat aattaattaa	900
aatcttactc tgtatatttc tgctaatacat tcactaaaca gcaaagaaaa acaaacacgt	960
atcatagata taaatgtaat ggcatagtgc gggtttttatt ttcagcctgt atcgtagcta	1020
aacaaatcga gttgtgggtc cgttttgggg cgttctgcc aattgttttag agtttcttga	1080
ataaatgtac gttctaaatt aaacgaagct gtcagcgcct ttatatagct ttctcgttct	1140
tcttttttta atttaatgat cgatagcaac aatgatttaa cactagcaag ttgaatgcc a	1200
ccatttcttc ctggtttaat cttaaagaaa atttcctgat tcgccttcag taccttcagc	1260
aatttatcta atgtccgttc aggaatgcct agcacttctc taatctcttt tttggtcgtc	1320
gctaaataag gcttgatac atcgcttttt tcgctaatat aagccattaa atcttctttc	1380
cattctgaca aatgaacacg ttgacgttcg cttctttttt tcttgaattt aaaccacct	1440
tgacggacaa ataaatcttt actggttaaa tcacttgata cccaagcttt gcaaagaatg	1500
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